<110> CropDesign N.V.

<120> Seedy1 sequence for making plants having changed growth characteristics

<130> CD-105-PCT

<150> US 60/528,113
<151> 2003-12-09

<150> EP 03104280.7
<151> 2003-11-19

<160> 18

<170> PatentIn version 3.3

<210> 1
<211> 1428
<212> DNA
<213> Nicotiana tabacum

<220>
<221> misc_feature
<223> seedy1 coding sequence (CDS0689)

<400> 1

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ctgaaacccc tttcggttag gccatcagat tcctttgaat ctgatttgtc aagtaaggaa     180

aatcaaactc ctttatttga gaattcatct gttaatctct catctccgtt acccataaag     240

ccacttaacc ctaatggggc tctggaaaat tcaagactca agccgaacaa gcccaattcc     300

aaacagagtc ttgatgagat ggcggctaga aagagcggaa agggaaatga tttccgtgat     360

gagaagaaaa tagacaggga aattgaagaa attcagatgg agattagtag gttgagttca     420

agattagagg ctttgagaat tgaaaaggct gagaaaactg ttgctaagac tgttgaaaag     480

cgaggaaggg ttgtggcagc aaagtttatg agccaaaac aaagtgttat taagattgaa     540

gagcgtatat caatgagtgc aagaacaaag gtggagcaga aaggggtct tagtttagga     600

ccatctgaga tttttactgg aacgcggcgg cgagggttga gtatgggggcc atcagatatt     660
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Page 1

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acaaggcagg cagttactac aattgcatca aagaagaatt tgaaaaaaga tgatggactt      900

ttgagttcag ttcagccaaa gaagttgttt aaagatctcg aaaagtctgc tgctgctaat      960

aagaagcccc agaggccggg gagggttgtg gctagtaggt ataatcagag tacaattcag     1020

tcatcagtag tgagaaagag gtctttacct gaaaatgata aggatgagag taagagaaat     1080

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ggaaacacag agagtgagaa atctccacta agcattattg tgaagcctga tttgcttccg     1260

cgaattagga ttgctcggtg tgtgaatgag actcttaggg attctggacc tgctaaaaga     1320

atgatagagt tgataggcaa gaaatcgttt ttcagtagtg atgaagataa ggagccacct     1380

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<210> 2
<211> 475
<212> PRT
<213> Nicotiana tabacum

<220>
<221> MISC_FEATURE
<223> seedy1 protein (CDS0689)

<400> 2

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Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Asp Ser Glu Asp Leu Ser
                20                  25                  30

Ser Leu Lys Arg Ser Trp Ser Pro Leu Lys Pro Leu Ser Val Arg Pro
        35                  40                  45

Ser Asp Ser Phe Glu Ser Asp Leu Ser Ser Lys Glu Asn Gln Thr Pro
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             50   55   60

Leu Phe Glu Asn Ser Ser Val Asn Leu Ser Ser Pro Leu Pro Ile Lys
65   70   75   80

Pro Leu Asn Pro Asn Gly Ala Leu Glu Asn Ser Arg Leu Lys Pro Asn
                  85   90   95

Lys Pro Asn Ser Lys Gln Ser Leu Asp Glu Met Ala Ala Arg Lys Ser
                  100   105   110

Gly Lys Gly Asn Asp Phe Arg Asp Glu Lys Lys Ile Asp Glu Glu Ile
              115   120   125

Glu Glu Ile Gln Met Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu Ala
          130   135   140

Leu Arg Ile Glu Lys Ala Glu Lys Thr Val Ala Lys Thr Val Glu Lys
145   150   155   160

Arg Gly Arg Val Val Ala Ala Lys Phe Met Glu Pro Lys Gln Ser Val
                  165   170   175

Ile Lys Ile Glu Glu Arg Ile Ser Met Ser Ala Arg Thr Lys Val Glu
              180   185   190

Gln Arg Arg Gly Leu Ser Leu Gly Pro Ser Glu Ile Phe Thr Gly Thr
          195   200   205

Arg Arg Arg Gly Leu Ser Met Gly Pro Ser Asp Ile Leu Ala Gly Thr
      210   215   220

Thr Lys Ala Arg Gln Leu Gly Lys Gln Glu Met Ile Ile Thr Pro Ile
225   230   235   240

Gln Pro Ile Gln Asn Arg Arg Lys Ser Cys Phe Trp Lys Leu Gln Glu
                  245   250   255

Ile Glu Glu Glu Gly Lys Ser Ser Ser Leu Ser Pro Lys Ser Arg Lys

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Thr Ala Ala Arg Thr Met Val Thr Thr Arg Gln Ala Val Thr Thr Ile
         275   280   285

Ala Ser Lys Lys Asn Leu Lys Lys Asp Asp Gly Leu Leu Ser Ser Val
    290   295   300

Gln Pro Lys Lys Leu Phe Lys Asp Leu Glu Lys Ser Ala Ala Ala Asn
305   310   315   320

Lys Lys Pro Gln Arg Pro Gly Arg Val Val Ala Ser Arg Tyr Asn Gln
             325   330   335

Ser Thr Ile Gln Ser Ser Val Val Arg Lys Arg Ser Leu Pro Glu Asn
             340   345   350

Asp Lys Asp Glu Ser Lys Arg Asn Asp Lys Lys Arg Ser Leu Ser Val
         355   360   365

Gly Lys Thr Arg Val Ser Gln Thr Glu Ser Lys Asn Leu Gly Thr Glu
    370   375   380

Ser Arg Val Lys Lys Arg Trp Glu Ile Pro Ser Glu Ile Val Val His
385   390   395   400

Gly Asn Thr Glu Ser Glu Lys Ser Pro Leu Ser Ile Ile Val Lys Pro
             405   410   415

Asp Leu Leu Pro Arg Ile Arg Ile Ala Arg Cys Val Asn Glu Thr Leu
         420   425   430

Arg Asp Ser Gly Pro Ala Lys Arg Met Ile Glu Leu Ile Gly Lys Lys
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Ser Phe Phe Ser Ser Asp Glu Asp Lys Glu Pro Pro Val Cys Gln Val
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Leu Ser Phe Ala Glu Glu Asp Ala Glu Glu Glu
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<212>   DNA
<213>   Oryza sativa

<220>
<221>   misc_feature
<223>   seedy1 coding sequence

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gccgagatcg ccacatcgga ggcggagatc ctgcgcctct cgtcccggct ccaccatctc     240

cgcgtctcca agcagccgga gcccaaccgc gacgacgctc cgatggggga gatggtcgcg     300

aaggtgaggc cccggccgag gggcctcagc ctcgggcccc tggatgtgat ctccatcgtc     360

aatcgtgaga agcatccgct gcgcaccaag cagcctccgg cgacgcgggg caggggggctc     420

agcctcgggc ccatggagat cgccgcggcg aaccctaggg tgcccgcggc ggcgcagcat     480

cagcaacagc aacgcgctgg cacggcgcgg atcctgaagc caatcaagga gcctccggtg     540

cagcgtcgca ggggcgtcag cctcgggccg ttggagatcc accacgcgt cggcagcaag      600

gcaccagcgg cggcgcgagc caagccgttc accaccaagc tcaacgccat tcgagaagaa     660

acccgaccct ccaagcaatt cgccgtcccc gccaagccat ggccgtcgag caatacaagg     720

cagacactgg actcgaggca aggaacagca gcaagtcgag cgaaggcgag gagcccgagc     780

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gtggatgagc tcaagcccaa aggtcgtcg tcaagtcaga gcggcagcgc cgccgccgcc       900

gccactgcca agaggatggc ggggagctcc aagatgaggg tcatcccgag ccgctacagc     960

ctcactcctg cgcgcttccct tggaagcagt ggagcacagg agaggcgacg caagcagtct    1020

ctcccaggat catcagggga tgcgaaccaa aatgaggaaa tcagagcgaa ggtcatcgag    1080

ccttccaatg atccactctc tcctcaaacg atctctcaag ttgctgaaat gctcccaaag    1140
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atcaggacca tgccgcctcc tgacgagagc cctcgcgatt ccggatgcgc caagcgggtt   1200

gccgaattgg tcgggaagcg ctcgttcttc acggctgcag ccgaggacgg gcgggcgctc   1260

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<212>   PRT
<213>   Oryza sativa

<220>
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<223>   seedy1 protein

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Ala Phe Asp Asp Ser Ser Cys Ser Arg Ser Ala Trp Leu Pro Gln Ser
            20   25   30

Pro Ala Val Ala Ala Val Arg Lys Gly Asp Lys Glu Asn His Arg Pro
        35   40   45

Glu Val Val Asp Val Ala Ala Gly Tyr Asp Val Glu Ala Glu Ile Gly
    50   55   60

His Ile Glu Ala Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu
65   70   75   80

Arg Val Ser Lys Gln Pro Glu Pro Asn Arg Asp Asp Ala Pro Met Gly
                85   90   95

Glu Met Val Ala Lys Val Arg Pro Arg Pro Arg Gly Leu Ser Leu Gly
            100   105   110

Pro Leu Asp Val Ile Ser Ile Val Asn Arg Glu Lys His Pro Leu Arg
        115   120   125

Thr Lys Gln Pro Pro Ala Thr Arg Gly Arg Gly Leu Ser Leu Gly Pro
   130   135   140

Met Glu Ile Ala Ala Ala Asn Pro Arg Val Pro Ala Ala Ala Gln His
145   150   155   160

Gln Gln Gln Gln Arg Ala Gly Thr Ala Arg Ile Leu Lys Pro Ile Lys
          165   170   175

Glu Pro Pro Val Gln Arg Arg Arg Gly Val Ser Leu Gly Pro Leu Glu
        180   185   190

Ile His His Gly Val Gly Ser Lys Ala Pro Ala Ala Ala Arg Ala Lys
       195   200   205

Pro Phe Thr Thr Lys Leu Asn Ala Ile Arg Glu Glu Thr Arg Pro Ser
   210   215   220

Lys Gln Phe Ala Val Pro Ala Lys Pro Trp Pro Ser Ser Asn Thr Arg
225   230   235   240

Gln Thr Leu Asp Ser Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala
        245   250   255

Arg Ser Pro Ser Pro Arg Pro Arg Arg Gln Ser Asn Gly Lys Ala Thr
        260   265   270

Asp Thr Arg Gly Gly Asn Lys Val Val Asp Glu Leu Lys Pro Lys Gly
       275   280   285

Ala Ser Ser Ser Gln Ser Gly Ser Ala Ala Ala Ala Thr Ala Lys
   290   295   300

Arg Met Ala Gly Ser Ser Lys Met Arg Val Ile Pro Ser Arg Tyr Ser
305   310   315   320

Leu Thr Pro Gly Ala Ser Leu Gly Ser Ser Gly Ala Gln Glu Arg Arg
        325   330   335

Arg Lys Gln Ser Leu Pro Gly Ser Ser Gly Asp Ala Asn Gln Asn Glu
          340   345   350

Glu Ile Arg Ala Lys Val Ile Glu Pro Ser Asn Asp Pro Leu Ser Pro
          355   360   365

Gln Thr Ile Ser Lys Val Ala Glu Met Leu Pro Lys Ile Arg Thr Met
     370   375   380

Pro Pro Pro Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg Val
385   390   395   400

Ala Glu Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Ala Glu Asp
          405   410   415

Gly Arg Ala Leu Asp Val Glu Ala Pro Glu Ala Val Ala Glu Ala
          420   425   430

<210>   5
<211>   1860
<212>   DNA
<213>   Medicago trunculata

<220>
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<223>   seedy1 coding sequence

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tttatttctt ccctcttcaa tctccaacgg tcacataatc tcttccaaat acaaataatt   240

ccctctttca acctcactct tcatttcttc aacccaaacc caaaaaacta atcagattct   300

tcttaaatct tgaaaccttt ctcccaaaag cacttaaaata aaaaagcact taaccatgaa   360

taacacaaac aacaacaaca ttcttcttca ttccacacag gttcaagtgt ggaacaacgc   420

agcattcgat ggtgaagatt tcgccatgaa ttcatcttct gattccatca aagagaatct   480

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aaacccatcc gcattcaaca ttgttccttc ttcaaacaaa agaactattg atgatgaaat    540

tgcggaaatt gaaagtgaaa ttaagcgatt aacttcgaag ctggaattgc ttcgtgttga    600

aaaagctgaa agaaaaatcg cttctgaaaa gcgtgttagt ggaattggta ctggaagaat    660

agtagcagcg aagtttatgg aaccgaagaa aaacgttaca ccgaaacgaa acggtgtcgt    720

tttcaaggag gagacaccga aacgaaacgg tgtcgtttcg gatacgccga aatctagggt    780

taattggaga agagggatga gtttaggtcc gatggagatt gccgggaaag tgatggcacc    840

gccggcgatg acgattactc cggcgacggt gaatcggagg aagtcttgtt tctggaaacc    900

gcaggaaagt tgtgaagtaa tgccgtcggg gattactccg cgacggtga ataggaggaa     960

atcttgtttt ttgaaacctc aagaaagttg tgaagaaaat cgaagaaaaa cgatttgcaa   1020

accgaatttg aatttgaatt caaattcagt taattctgcg gttggatcga ttaagcgtgt   1080

gaagaagaaa gatgaagaaa ttgctcaggt tcaaccgaag aagctgtttg aaggtgaaaa   1140

atcagtgaag aaatcgttga aacaaggtag aattgttgca agccggtata attccggtgg   1200

tggtggtggt gatgcgagga aaagatcgtt ttcggagaat aataagggtt tagggagtga   1260

aatcagggct aagaagagat gggagatacc aattgaagaa gtggatgtga gtggttttgt   1320

tatgttaccg aagatttcga caatgaggtt tgttgatgag agtcctagag attctggtgc   1380

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agatgatgat gatgatgatg attatggtga acaagggtaa ttgtggaaat tggaattgat   1560

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tgaaataata acaacaagca tgtgtcttgc ttaataattg tatattgttt tgtttgtttt   1740

ataatgatat ggatttaatt tgtatacaca atataatata gtatgcattg agagagtttt   1800

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<212>   PRT
<213>   Medicago trunculata

Page 9

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<223>   seedy1 protein

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Gln Val Trp Asn Asn Ala Ala Phe Asp Gly Glu Asp Phe Ala Met Asn
                20                  25                  30

Ser Ser Ser Asp Ser Ile Lys Glu Asn Leu Asn Pro Ser Ala Phe Asn
            35                  40                  45

Ile Val Pro Ser Ser Asn Lys Arg Thr Ile Asp Asp Glu Ile Ala Glu
    50                  55                  60

Ile Glu Ser Glu Ile Lys Arg Leu Thr Ser Lys Leu Glu Leu Leu Arg
65                  70                  75                  80

Val Glu Lys Ala Glu Arg Lys Ile Ala Ser Glu Lys Arg Val Ser Gly
                85                  90                  95

Ile Gly Thr Gly Arg Ile Val Ala Ala Lys Phe Met Glu Pro Lys Lys
                100                 105                 110

Asn Val Thr Pro Lys Arg Asn Gly Val Val Phe Lys Glu Glu Thr Pro
            115                 120                 125

Lys Arg Asn Gly Val Val Ser Asp Thr Pro Lys Ser Arg Val Asn Trp
        130                 135                 140

Arg Arg Gly Met Ser Leu Gly Pro Met Glu Ile Ala Gly Lys Val Met
145                 150                 155                 160

Ala Pro Pro Ala Met Thr Ile Thr Pro Ala Thr Val Asn Arg Arg Lys
                165                 170                 175

Ser Cys Phe Trp Lys Pro Gln Glu Ser Cys Glu Val Met Pro Ser Gly
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                    180   185   190

Ile Thr Pro Ala Thr Val Asn Arg Arg Lys Ser Cys Phe Leu Lys Pro
        195   200   205

Gln Glu Ser Cys Glu Glu Asn Arg Arg Lys Thr Ile Cys Lys Pro Asn
    210   215   220

Leu Asn Leu Asn Ser Asn Ser Val Asn Ser Ala Val Gly Ser Ile Lys
225   230   235   240

Arg Val Lys Lys Lys Asp Glu Glu Ile Ala Gln Val Gln Pro Lys Lys
                245   250   255

Leu Phe Glu Gly Glu Lys Ser Val Lys Lys Ser Leu Lys Gln Gly Arg
            260   265   270

Ile Val Ala Ser Arg Tyr Asn Ser Gly Gly Gly Gly Asp Ala Arg
        275   280   285

Lys Arg Ser Phe Ser Glu Asn Asn Lys Gly Leu Gly Ser Glu Ile Arg
    290   295   300

Ala Lys Lys Arg Trp Glu Ile Pro Ile Glu Glu Val Asp Val Ser Gly
305   310   315   320

Phe Val Met Leu Pro Lys Ile Ser Thr Met Arg Phe Val Asp Glu Ser
            325   330   335

Pro Arg Asp Ser Gly Ala Val Lys Arg Val Ala Glu Leu Asn Gly Lys
            340   345   350

Arg Ser Tyr Phe Cys Asp Glu Asp Glu Glu Glu Arg Val Met Val Glu
        355   360   365

Glu Glu Gly Gly Ser Val Cys Gln Val Leu Asn Phe Ala Glu Asp Asp
    370   375   380

Asp Asp Asp Asp Asp Tyr Gly Glu Gln Gly

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<212>   DNA
<213>   Saccharum sp.

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<223>   seedy1 coding sequence (partial 5' end)

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<222>   (362)..(362)
<223>   n can be a, c, g or t

<220>
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<222>   (372)..(372)
<223>   n can be a, c, g or t

<220>
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<222>   (674)..(674)
<223>   n can be a, c, g or t
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gaagcaggaa tccctccgct cccagccgcc tcctccgctc acccatcgat cgatcgtccg     120
tccggtccag ggggctctcc ggcggcggtg gcgatggagg aggacccgct catcccgctg     180
gtgcacgtct ggaacaacgc cgccttcgac cacgcctcct cctccgcgtg gcacgcccac     240
tcccctgtgc ccgcgagcgc acgtcgcgag gcggagggggg acaaggagaa ccaccgcccc    300
gaccccgacc ccgacgtcga ggcggagatc ggccacatcg aggcggagat cctgcgcctg     360
tnctcccgcc tncaccacct tcgcacctcc aagcagtcgg agccgtccaa gcgcggagag     420
gtcgcgcccg cgcccgcggc gaaggcgaaa gcggcggcgg cggcgcggct gcggacgcgg     480
gggctcagcc tgggcccgct cgacgtcgcc gctgccggta acccaaccc gctcaccacc      540
gacaaccagc agcagcagcc gcgtgccgcg caggtctga agccgatcaa gcaggccacg      600
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<210>   8
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<212>   PRT
<213>   Saccharum sp.


<220>
<221>   MISC_FEATURE
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<220>
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<223>   seedy1 protein (partial N term)

<220>
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<222>   (70)..(70)
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Ala Phe Asp His Ala Ser Ser Ser Ala Trp His Ala His Ser Pro Val
                20   25   30

Pro Ala Ser Ala Arg Arg Glu Ala Glu Gly Asp Lys Glu Asn His Arg
            35   40   45

Pro Asp Pro Asp Pro Asp Val Glu Ala Glu Ile Gly His Ile Glu Ala
        50   55   60

Glu Ile Leu Arg Leu Xaa Ser Arg Leu His His Leu Arg Thr Ser Lys
65   70   75   80

Gln Ser Glu Pro Ser Lys Arg Gly Glu Val Ala Pro Ala Pro Ala Ala
                85   90   95

Lys Ala Lys Ala Ala Ala Ala Ala Arg Leu Arg Thr Arg Gly Leu Ser
            100   105   110

Leu Gly Pro Leu Asp Val Ala Ala Ala Gly Asn Pro Asn Pro Leu Thr

| | 115 | | 120 | | 125 |

Thr Asp Asn Gln Gln Gln Gln Pro Arg Ala Ala Gln Gly Leu Lys Pro
   130   135   140

Ile Lys Gln Ala Thr Ala Ala Ala Gly Lys Gly Val Arg Leu Gly Pro
145   150   155   160

Leu Arg His Gly Arg Arg
                165

<210> 9
<211> 876
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<223> seedy1 coding sequence (partial 3' end)

<220>
<221> misc_feature
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<223> n = a, c, g or t

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caagcagagc caaggcgagg agcgggagca taagcccca gcaggttcag aggcagtcca   180
cttccaaggc tgccgagaca agagcgggaa atgccaagcc tacagaggcg acgaggggag   240
ggagcgaagc ggtcaatcac accagcaatg tagccacgac gaagaggccg gcggggagct   300
ccaaggtcag ggttgtcccg agccgctaca gcatcccacc tggctcctcc ctagcagctg   360
tgacacaagg caaccgatgc aagcagtctc tcccaggatc ggctactgag accagagtaa   420
atctcactga gccgccgaac gacgagttgt ctcctgaaga acttgccaag gttgcagagc   480
tgctcccaag gattaggacc atgccgcctt ctgatgagag cccgcgtgac tcgggatgtg   540
ccaagcgtgt tgctgatttg gtcgggaagc gatccttctt cactgctgca ggggacgatg   600
gcaatctcgt tacgccctac caggcacggg tggttgaact tgaatcaccc gaggcagcag   660

cagaagaagc agaagcttga gaagtttgtc tttgatcaat tccgaagtgg cttgcatctg   720

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tcacatttcc tattttttcc cccttgagac attgcttagt acttttgtgt tgccttgtga   840

aaagagagtg gaaggttcat ctgctgatnc cttgtt   876

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<211>   224
<212>   PRT
<213>   Zea mays

<220>
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<223>   seedy1 protein (partial C term)

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Thr Arg Pro Ala Val Arg Glu Glu Glu Gly Gln Arg Ser Lys Glu His
1   5   10   15

Ala Val Pro Ala Arg Pro Trp Pro Ser Ser Asn Ala Arg His Pro Leu
                20   25   30

Asp Ala Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala Arg Ser Gly
            35   40   45

Ser Ile Ser Pro Ser Arg Phe Arg Arg Gln Ser Thr Ser Lys Ala Ala
        50   55   60

Glu Thr Arg Ala Gly Asn Ala Lys Pro Thr Glu Ala Thr Arg Gly Gly
65   70   75   80

Ser Glu Ala Val Asn His Thr Ser Asn Val Ala Thr Thr Lys Arg Pro
                85   90   95

Ala Gly Ser Ser Lys Val Arg Val Val Pro Ser Arg Tyr Ser Ile Pro
                100   105   110

Pro Gly Ser Ser Leu Ala Ala Val Thr Gln Gly Asn Arg Cys Lys Gln
            115   120   125

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Ser Leu Pro Gly Ser Ala Thr Glu Thr Arg Val Asn Leu Thr Glu Pro
    130             135             140

Pro Asn Asp Glu Leu Ser Pro Glu Glu Leu Ala Lys Val Ala Glu Leu
145             150             155             160

Leu Pro Arg Ile Arg Thr Met Pro Pro Ser Asp Glu Ser Pro Arg Asp
            165             170             175

Ser Gly Cys Ala Lys Arg Val Ala Asp Leu Val Gly Lys Arg Ser Phe
            180             185             190

Phe Thr Ala Ala Gly Asp Asp Gly Asn Leu Val Thr Pro Tyr Gln Ala
            195             200             205

Arg Val Val Glu Leu Glu Ser Pro Glu Ala Ala Ala Glu Glu Ala Glu
    210             215             220
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<210> 11
<211> 1257
<212> DNA
<213> Arabidopsis thaliana

<220>
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<223> seedy1 coding sequence

<400> 11
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tctcacctca cgaatcatt cgattccgat tgtagcaagg agaatcagtt ccgatttcg    180
gtttcctctt cgctccaatc ctcagtctcg atcaccgaag ctccgtcagc aaaatccaag   240
accgtgaaga ccaaatccgc cgcagatcgg agtaaaaagc gagatatcga tgcagagatc   300
gaagaagtag agaaggagat cggacgatta tcgacgaaat tggagtcgct ccgattagag   360
aaggcggagc aaaccgcaag aagcattgct atacgtggaa gaatcgttcc ggcgaagttc   420
atggaatcat ctcagaaaca agtgaaattc gacgattcgt gttttacagg atcgaaatca   480
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agagccactc gtagaggcgt tagtcttgga ccagcggaga tattcaattc cgcgaagaaa    540

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ctgagtccga gatctcgcaa agcgaaaatg acggcagctc agaagcaagc agctacgacg    720

gtggggtcaa agagagctgt gaagaaagaa gaaggagttc tcttaacaat ccagcctaag    780

aggctattca aagaagatga aaagaatgtt tctttaagga aaccattgaa accaggaaga    840

gttgtggcta gtaggtacag tcaaatgggt aaaacgcaga ctggagagaa agatgttagg    900

aaaaggtcgt tgcctgagga tgaagagaaa gagaatcata agaggtcgga gaagagaaga    960

gcttctgatg aaagtaacaa gagtgaaggg agagtgaaga agagatggga gattccaagt   1020

gaagttgatc tgtatagcag tggtgagaac ggtgacgagt ctcctatagt taaggagcta   1080

cctagatca gaacgcttcg tcgtgtggga gggagccctc gtgattcagg tgctgctaag   1140

agagttgcag aattacaagc caaggatcga aacttcactt tttgccagct tctgaagttt   1200

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<220>
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<223>  seedy1 protein

<400>  12
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Gln Ile Trp Asn Asn Ala Ala Phe Asp Asp Gly Asp Ser Gln Ile Thr
                20                  25                  30

Ser Ala Ile Glu Ala Ser Ser Trp Ser His Leu Asn Glu Ser Phe Asp
        35                  40                  45
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Ser Asp Cys Ser Lys Glu Asn Gln Phe Pro Ile Ser Val Ser Ser Ser
    50   55   60

Leu Gln Ser Ser Val Ser Ile Thr Glu Ala Pro Ser Ala Lys Ser Lys
65   70   75   80

Thr Val Lys Thr Lys Ser Ala Ala Asp Arg Ser Lys Lys Arg Asp Ile
                85   90   95

Asp Ala Glu Ile Glu Glu Val Glu Lys Glu Ile Gly Arg Leu Ser Thr
                100   105   110

Lys Leu Glu Ser Leu Arg Leu Glu Lys Ala Glu Gln Thr Ala Arg Ser
            115   120   125

Ile Ala Ile Arg Gly Arg Ile Val Pro Ala Lys Phe Met Glu Ser Ser
    130   135   140

Gln Lys Gln Val Lys Phe Asp Asp Ser Cys Phe Thr Gly Ser Lys Ser
145   150   155   160

Arg Ala Thr Arg Arg Gly Val Ser Leu Gly Pro Ala Glu Ile Phe Asn
                165   170   175

Ser Ala Lys Lys Ser Glu Thr Val Thr Pro Leu Gln Ser Ala Gln Asn
            180   185   190

Arg Arg Lys Ser Cys Phe Phe Lys Leu Pro Gly Ile Glu Glu Gly Gln
            195   200   205

Val Thr Thr Arg Gly Lys Gly Arg Thr Ser Leu Ser Leu Ser Pro Arg
    210   215   220

Ser Arg Lys Ala Lys Met Thr Ala Ala Gln Lys Gln Ala Ala Thr Thr
225   230   235   240

Val Gly Ser Lys Arg Ala Val Lys Lys Glu Glu Gly Val Leu Leu Thr
                245   250   255

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Ile Gln Pro Lys Arg Leu Phe Lys Glu Asp Glu Lys Asn Val Ser Leu
            260                 265                 270

Arg Lys Pro Leu Lys Pro Gly Arg Val Val Ala Ser Arg Tyr Ser Gln
            275                 280                 285

Met Gly Lys Thr Gln Thr Gly Glu Lys Asp Val Arg Lys Arg Ser Leu
    290                 295                 300

Pro Glu Asp Glu Glu Lys Glu Asn His Lys Arg Ser Glu Lys Arg Arg
305                 310                 315                 320

Ala Ser Asp Glu Ser Asn Lys Ser Glu Gly Arg Val Lys Lys Arg Trp
            325                 330                 335

Glu Ile Pro Ser Glu Val Asp Leu Tyr Ser Ser Gly Glu Asn Gly Asp
            340                 345                 350

Glu Ser Pro Ile Val Lys Glu Leu Pro Lys Ile Arg Thr Leu Arg Arg
            355                 360                 365

Val Gly Gly Ser Pro Arg Asp Ser Gly Ala Ala Lys Arg Val Ala Glu
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Glu Glu
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aaacaagagt gtcaatggaa caatgaaaac catatgacat actataattt tgtttttatt     240

attgaaatta tataattcaa agagaataaa tccacatagc cgtaaagttc tacatgtggt     300

gcattaccaa aatatatata gcttacaaaa catgacaagc ttagtttgaa aaattgcaat     360

ccttatcaca ttgacacata aagtgagtga tgagtcataa tattattttc tttgctaccc     420

atcatgtata tatgatagcc acaaagttac tttgatgatg atatcaaaga acatttttag     480

gtgcacctaa cagaatatcc aaataaatatg actcacttag atcataatag agcatcaagt     540

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aatcctcatc atccttcacc acaattcaaa tattatagtt gaagcatagt agtaatttaa     660

atcaactagg gatatcacaa gtttgtacaa aaaagcaggc tggtaccggt ccggaattcc     720

cgggatatcg tcgacccacg cgtccgctga cgcgtgggtt ccactacatc aagacatcta     780

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agcatttgat aatggagatt ctgaagattt gtcttgctg aaacgttctt ggtctcctct     960

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tcaaactcct ttatttgaga attcatctgt taatctctca tctccgttac ccataaagcc    1080

acttaaccct aatggggctc tggaaaattc aagactcaag ccgaacaagc ccaattccaa    1140

acagagtctt gatgagatgg cggctagaaa gagcggaaag ggaaatgatt tccgtgatga    1200

gaagaaaata gacgaggaaa ttgaagaaat tcagatggag attagtaggt tgagttcaag    1260

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atcagtagtg agaaagaggt ctttacctga aaatgataag gatgagagta agagaaatga    1920

taagaaacgg tcgttatctg tagggaaaac gcgtgtgtct caaactgaga gcaagaattt    1980

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cacacaacaa ataagagaaa aaacaaataa tattaatttg agaatgaaca aaaggaccat    2940

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gttattgtaa agttctacaa agctaattta aaagttattg cattaactta tttcatatta     180

caaacaagag tgtcaatgga acaatgaaaa ccatatgaca tactataatt ttgttttttat    240

tattgaaatt atataattca aagagaataa atccacatag ccgtaaagtt ctacatgtgg     300

tgcattacca aaatatatat agcttacaaa acatgacaag cttagtttga aaaattgcaa      360

tccttatcac attgacacat aaagtgagtg atgagtcata atattatttt tcttgctacc     420

catcatgtat atatgatagc cacaaagtta ctttgatgat gatatcaaag aacatttttta    480

ggtgcaccta acagaatatc caaataatat gactcactta gatcataata gagcatcaag     540

taaaactaac actctaaagc aaccgatggg aaagcatcta taaatagaca agcacaatga     600

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caacaaca                                                               668


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<220>
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<210> 17
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<400>  17
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1   5   10   15

Xaa Xaa Leu Arg
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<220>
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<220>
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<223>   Xaa can be any amino acid within a stretch of 1 to 6 amino acids

<400>   18

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1   5   10   15

Ser Gly Xaa Xaa Lys Arg Xaa Xaa Xaa Xaa Xaa Xaa Lys
            20   25